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				Application Number	10/032,281
				Filing Date	December 21, 2001
				First Named Inventor	WYRICK, JOHN
				Art Unit	1637
				Examiner Name	Horlick, Kenneth R
				Attorney Docket Number	WTHD-007CIP
Sheet	1	of	3		

[illegible][illegible]

Examiner Signature		Date Considered	
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This collection of information is required by 37 CFR 1.97 and 1.98. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 2 hours to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. **SEND TO: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.**

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NON PATENT LITERATURE DOCUMENTS			
Examiner Initials*	Cite No. ¹	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published.	T ²
		BARNARD, et al. PCR bias toward the wild-type k-ras and p53 sequences: Implications for PCR detection of mutations and cancer diagnosis. BioTechniques. 1998, vol. 25, no. 4, pp 684-691.	
		BECKER, et al. PCR bias in ecological analysis: a case study for quantitative Taq nuclease assays in analyses of microbial communities. Applied and Environmental Microbiology. 2004, vol. 66, no. 11, pp. 4945-4953.	
		Jl, et al. Preservation of gene expression ratios among multiple complex cDNAs after PCR amplification: Application to differential gene expression studies. Journal of Structural and Functional Genomics. 2000, vol. 1, pp. 1-7.	
		KANAGAWA. Review: Bias and artifacts in multitemplate polymerase chain reactions (PCR). Journal of Bioscience and Bioengineering. 2003, vol. 96, no. 4, pp. 317-323.	
		LIU, et al. Inhibition of PCR amplification by a point mutation downstream of a primer. BioTechniques. 1997, vol. 22, no. 2, pp. 292-300.	
		LOCKHART, et al. Genomics, gene expression and DNA arrays. Nature. 2000, vol. 405, pp. 827-836.	
		LUEDERS, et al. Evaluation of PCR amplification bias by terminal restriction fragment length polymorphism analysis of small-subunit rRNA and mcrA genes by using defined template mixtures of methanogenic pure cultures and soil DNA extracts. Applied and Environmental Microbiology. 2003, vol. 69, no. 1, pp. 320-326.	
		MATHIEU-DAUDE, et al. DNA rehybridization during PCR: the 'C ₀ t' effect' and its consequences. Nucleic Acids Research. 1996, vol. 24, no. 11, pp. 2080-2086.	
		POLZ, et al. Bias in template-to-product ratios in multitemplate PCR. Applied and Environmental Microbiology. 1998, vol. 64, pp. 3724-3730.	
		SCHWABE, et al. High-copy cDNA amplification of minimal total RNA quantities for gene expression analyses. Molecular Biotechnology. 2000, vol. 14, pp. 165-172.	

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		SUZUKI, et al. Kinetic bias in estimates of coastal picoplankton community structure obtained by measurements of small-subunit rRNA gene PCR amplicon length heterogeneity. Applied and Environmental Microbiology. 1998, vol. 64, no. 11, pp. 4522-4529.	
		WADENBACK, et al. Comparison of standard exponential and linear techniques to amplify small cDNA samples for microarrays. BMC Genomics. 2005, vol. 6:61.	
		WAGNER, et al. Surveys of gene families using polymerase chain reaction: PCR selection and PCR drift. Systematic Biology. 1994, vol. 43, pp. 250-261.	
		WARNECKE, et al. Detection and measurement of PCR bias in quantitative methylation analysis of bisulphite-treated DNA. Nucleic Acids Research. 1997, vol. 25, no. 21, pp. 4422-4426	
		WINTZINGERODE, et al. Determination of microbial diversity in environmental samples: pitfalls of PCR-based rRNA analysis. FEMS Microbiology Reviews. 1997, vol. 21, pp. 213-229.	

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